

## SEQUENCE LISTING

&lt;110&gt; SOLVAY PHARMACEUTICALS B.V.

5 &lt;120&gt; Novel human G-protein coupled receptor

&lt;130&gt; SPW99.04

&lt;140&gt;

10 &lt;141&gt;

&lt;160&gt; 18

&lt;170&gt; PatentIn Ver. 2.1

15

&lt;210&gt; 1

&lt;211&gt; 1659

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

20

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (36)..(1559)

25

&lt;400&gt; 1

gcctgcaacc tgtcycacgc cctctggetg ttgcc atg acg tcc acc tgc acc 53  
 Met Thr Ser Thr Cys Thr  
 1 5

30

aac agc acg cgc gag agt aac agc agc cac acg tgc atg ccc ctc tcc 101  
 Asn Ser Thr Arg Glu Ser Asn Ser Ser His Thr Cys Met Pro Leu Ser  
 10 15 20

35

aaa atg ccc atc agc ctg gcc cac ggc atc atc cgc tca acc gtg ctg 149  
 Lys Met Pro Ile Ser Leu Ala His Gly Ile Ile Arg Ser Thr Val Leu  
 25 30 35

40

gtt atc ttc ctc gcc gcc tct ttc gtc ggc aac ata gtg ctg gcg cta 197  
 Val Ile Phe Leu Ala Ala Ser Phe Val Gly Asn Ile Val Leu Ala Leu  
 40 45 50

45

gtg ttg cag cgc aag ccg cag ctg ctg cag gtg acc aac cgt ttt atc 245  
 Val Leu Gln Arg Lys Pro Gln Leu Leu Gln Val Thr Asn Arg Phe Ile  
 55 60 65 70

ttt aac ctc ctc gtc acc gac ctg ctg cag att tcg ctc gtg gcc ccc 293  
 Phe Asn Leu Leu Val Thr Asp Leu Leu Gln Ile Ser Leu Val Ala Pro  
 75 80 85

50

tgg gtg gtg gcc acc tct gtg cct ctc ttc tgg ccc ctc aac agc cac 341  
 Trp Val Val Ala Thr Ser Val Pro Leu Phe Trp Pro Leu Asn Ser His  
 90 95 100

55

SUBSTITUTE SHEET (RULE 26)

	ttc tgc acg gcc ctg gtt agc ctc acc cac ctg ttc gcc ttc gcc agc	389
	Phe Cys Thr Ala Leu Val Ser Leu Thr His Leu Phe Ala Phe Ala Ser	
	105 110 115	
5	gtc aac acc att gtc ttg gtg tca gtg gat cgc tac ttg tcc atc atc	437
	Val Asn Thr Ile Val Leu Val Ser Val Asp Arg Tyr Leu Ser Ile Ile	
	120 125 130	
10	cac cct ctc tcc tac ccg tcc aag atg acc cag cgc cgc ggt tac ctg	485
	His Pro Leu Ser Tyr Pro Ser Lys Met Thr Gln Arg Arg Gly Tyr Leu	
	135 140 145 150	
15	ctc ctc tat ggc acc tgg att gtg gcc atc ctg cag agc act cct cca	533
	Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile Leu Gln Ser Thr Pro Pro	
	155 160 165	
20	ctc tac ggc tgg ggc cag gct gcc ttt gat gag cgc aat gct ctc tgc	581
	Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp Glu Arg Asn Ala Leu Cys	
	170 175 180	
25	tcc atg atc tgg ggg gcc agc ccc agc tac act att ctc agc gtg gtg	629
	Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr Thr Ile Leu Ser Val Val	
	185 190 195	
30	tcc ttc atc gtc att cca ctg att gtc atg att gcc tgc tac tcc gtg	677
	Ser Phe Ile Val Ile Pro Leu Ile Val Met Ile Ala Cys Tyr Ser Val	
	200 205 210	
35	gtg ttc tgt gca gcc cgg agg cag cat gct ctg ctg tac aat gtc aag	725
	Val Phe Cys Ala Ala Arg Arg Gln His Ala Leu Leu Tyr Asn Val Lys	
	215 220 225 230	
40	aga cac agc ttg gaa gtg cga gtc aag gac tgt gtg gag aat gag gat	773
	Arg His Ser Leu Glu Val Arg Val Lys Asp Cys Val Glu Asn Glu Asp	
	235 240 245	
45	gaa gag gga gca gag aag aag gag gag ttc cag gat gag agt gag ttt	821
	Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe Gln Asp Glu Ser Glu Phe	
	250 255 260	
50	cgc cgc cag cat gaa ggt gag gtc aag gcc aag gag ggc aga atg gaa	869
	Arg Arg Gln His Glu Gly Glu Val Lys Ala Lys Glu Gly Arg Met Glu	
	265 270 275	
55	gcc aag gac ggc agc ctg aag gcc aag gaa gga agc acg ggg acc agt	917
	Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu Gly Ser Thr Gly Thr Ser	
	280 285 290	
60	gag agt agt gta gag gcc agg ggc agc gag gag gtc aga gag agc agc	965
	Glu Ser Ser Val Glu Ala Arg Gly Ser Glu Glu Val Arg Glu Ser Ser	
	295 300 305 310	
65	acg gtg gcc agc gac ggc agc atg gag ggt aag gaa ggc agc acc aaa	1013
	Thr Val Ala Ser Asp Gly Ser Met Glu Gly Lys Glu Gly Ser Thr Lys	
	315 320 325	

5 gtt gag gag aac agc atg aag gca gac aag ggt cgc aca gag gtc aac 1061  
 Val Glu Glu Asn Ser Met Lys Ala Asp Lys Gly Arg Thr Glu Val Asn  
 330 335 340  
 cag tgc agc att gac ttg ggt gaa gat ggc atg gag ttt ggt gaa gac 1109  
 Gln Cys Ser Ile Asp Leu Gly Glu Asp Gly Met Glu Phe Gly Glu Asp  
 345 350 355  
 10 gac atc aat ttc agt gag gat gac gtc gag gca gtg aac atc ccg gag 1157  
 Asp Ile Asn Phe Ser Glu Asp Asp Val Glu Ala Val Asn Ile Pro Glu  
 360 365 370  
 15 agc ctc cca ccc agt cgt cgt aac agc aac agc aac cct cct ctg ccc 1205  
 Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn Ser Asn Pro Pro Leu Pro  
 375 380 385 390  
 20 agg tgc tac cag tgc aaa gct gct aaa gtg atc ttc atc atc att ttc 1253  
 Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val Ile Phe Ile Ile Ile Phe  
 395 400 405  
 25 tcc tat gtg cta tcc ctg ggg ccc tac tgc ttt tta gca gtc ctg gcc 1301  
 Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys Phe Leu Ala Val Leu Ala  
 410 415 420  
 30 gtg tgg gtg gat gtc gaa acc cag gta ccc cag tgg gtg atc acc ata 1349  
 Val Trp Val Asp Val Glu Thr Gln Val Pro Gln Trp Val Ile Thr Ile  
 425 430 435  
 35 atc atc tgg ctt ttc ttc ctg cag tgc tgc atc cac ccc tat gtc tat 1397  
 Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys Ile His Pro Tyr Val Tyr  
 440 445 450  
 40 ggc tac atg cac aag acc att aag aag gaa atc cag gac atg ctg aag 1445  
 Gly Tyr Met His Lys Thr Ile Lys Lys Glu Ile Gln Asp Met Leu Lys  
 455 460 465 470  
 aag ttc ttc tgc aag gaa aag ccc ccg aaa gaa gat agc cac cca gac 1493  
 Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys Glu Asp Ser His Pro Asp  
 475 480 485  
 45 ctg ccc gga aca gag ggt ggg act gaa ggc aag att gtc cct tcc tac 1541  
 Leu Pro Gly Thr Glu Gly Gly Thr Glu Gly Lys Ile Val Pro Ser Tyr  
 490 495 500  
 gat tct gct act ttt cct tgaagttagt tctaaggcaa accttgaaaa 1589  
 Asp Ser Ala Thr Phe Pro  
 505  
 50 tcagtccttc agccacagct atttagagct ttaaaactac caggttcaat cactgggttat 1649  
 gctttctgtg 1659  
 55

<210> 2  
 <211> 508  
 <212> PRT  
 <213> Homo sapiens

5

<400> 2  
 Met Thr Ser Thr Cys Thr Asn Ser Thr Arg Glu Ser Asn Ser Ser His  
 1 5 10 15

10 Thr Cys Met Pro Leu Ser Lys Met Pro Ile Ser Leu Ala His Gly Ile  
 20 25 30

Ile Arg Ser Thr Val Leu Val Ile Phe Leu Ala Ala Ser Phe Val Gly  
 35 40 45

15

Asn Ile Val Leu Ala Leu Val Leu Gln Arg Lys Pro Gln Leu Leu Gln  
 50 55 60

20

Val Thr Asn Arg Phe Ile Phe Asn Leu Leu Val Thr Asp Leu Leu Gln  
 65 70 75 80

Ile Ser Leu Val Ala Pro Trp Val Val Ala Thr Ser Val Pro Leu Phe  
 85 90 95

25

Trp Pro Leu Asn Ser His Phe Cys Thr Ala Leu Val Ser Leu Thr His  
 100 105 110

Leu Phe Ala Phe Ala Ser Val Asn Thr Ile Val Leu Val Ser Val Asp  
 115 120 125

30

Arg Tyr Leu Ser Ile Ile His Pro Leu Ser Tyr Pro Ser Lys Met Thr  
 130 135 140

35

Gln Arg Arg Gly Tyr Leu Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile  
 145 150 155 160

Leu Gln Ser Thr Pro Pro Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp  
 165 170 175

40

Glu Arg Asn Ala Leu Cys Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr  
 180 185 190

45

Thr Ile Leu Ser Val Val Ser Phe Ile Val Ile Pro Leu Ile Val Met  
 195 200 205

Ile Ala Cys Tyr Ser Val Val Phe Cys Ala Ala Arg Arg Gln His Ala  
 210 215 220

50

Leu Leu Tyr Asn Val Lys Arg His Ser Leu Glu Val Arg Val Lys Asp  
 225 230 235 240

Cys Val Glu Asn Glu Asp Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe  
 245 250 255

55

SUBSTITUTE SHEET (RULE 26)

5 Gln Asp Glu Ser Glu Phe Arg Arg Gln His Glu Gly Glu Val Lys Ala  
 260 265 270  
 Lys Glu Gly Arg Met Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu  
 275 280 285  
 Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly Ser Glu  
 290 295 300  
 10 Glu Val Arg Glu Ser Ser Thr Val Ala Ser Asp Gly Ser Met Glu Gly  
 305 310 315 320  
 Lys Glu Gly Ser Thr Lys Val Glu Glu Asn Ser Met Lys Ala Asp Lys  
 325 330 335  
 15 Gly Arg Thr Glu Val Asn Gln Cys Ser Ile Asp Leu Gly Glu Asp Gly  
 340 345 350  
 20 Met Glu Phe Gly Glu Asp Asp Ile Asn Phe Ser Glu Asp Asp Val Glu  
 355 360 365  
 Ala Val Asn Ile Pro Glu Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn  
 370 375 380  
 25 Ser Asn Pro Pro Leu Pro Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val  
 385 390 395 400  
 30 Ile Phe Ile Ile Ile Phe Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys  
 405 410 415  
 Phe Leu Ala Val Leu Ala Val Trp Val Asp Val Glu Thr Gln Val Pro  
 420 425 430  
 35 Gln Trp Val Ile Thr Ile Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys  
 435 440 445  
 40 Ile His Pro Tyr Val Tyr Gly Tyr Met His Lys Thr Ile Lys Lys Glu  
 450 455 460  
 Ile Gln Asp Met Leu Lys Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys  
 465 470 475 480  
 45 Glu Asp Ser His Pro Asp Leu Pro Gly Thr Glu Gly Gly Thr Glu Gly  
 485 490 495  
 Lys Ile Val Pro Ser Tyr Asp Ser Ala Thr Phe Pro  
 500 505  
 50  
 <210> 3  
 <211> 27  
 <212> DNA  
 55 <213> Artificial Sequence

SUBSTITUTE SHEET (RULE 26)

<220>

<223> Description of Artificial Sequence:Primer

5

<220>

<221> variation

<222> (19)

<223> Degenerated primers

10

<220>

<221> variation

<222> (22)

<223> Degenerated primers

15

<220>

<221> variation

<222> (25)

<223> Degenerated primers

20

<400> 3

catcttcgtc gtcggcacng ynggnaa

27

25

<210> 4

<211> 26

<212> DNA

<213> Artificial Sequence

30

<220>

<223> Description of Artificial Sequence:Primer

<220>

<221> variation

<222> (21)

<223> Degenerated primers

35

<400> 4

gggtggcaga tggccarrya nkytc

26

40

<210> 5

<211> 27

<212> DNA

<213> Artificial Sequence

45

<220>

<223> Description of Artificial Sequence:Primer

<220>

<221> misc\_feature

<222> (27)

<223> Modified base : 3'-deoxyadenosine

50

<400> 5

acggtgggca acacggtgac ggcgtta

27

55

SUBSTITUTE SHEET (RULE 26)

5 <210> 6  
<211> 27  
<212> DNA  
<213> Artificial Sequence

10 <220>  
<223> Description of Artificial Sequence:Primer  
  
<400> 6  
ccatcctaata acgactcact atagggc

27

15 <210> 7  
<211> 23  
<212> DNA  
<213> Artificial Sequence

20 <220>  
<223> Description of Artificial Sequence:Primer  
  
<400> 7  
actcactata gggctcgagc ggc

23

25 <210> 8  
<211> 28  
<212> DNA  
30 <213> Artificial Sequence

35 <220>  
<223> Description of Artificial Sequence:Primer  
  
<400> 8  
tttatcttta acctcctcgt caccgacc

28

40 <210> 9  
<211> 20  
<212> DNA  
<213> Artificial Sequence

45 <220>  
<223> Description of Artificial Sequence:Primer  
  
<400> 9  
tagtggttgca gcgcaagccg

20

50 <210> 10  
<211> 30  
<212> DNA  
55 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:Primer

&lt;400&gt; 10

5 ggcagcgttc cactgacacc aagacaatgg

30

&lt;210&gt; 11

&lt;211&gt; 28

10 &lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

15 &lt;223&gt; Description of Artificial Sequence:Primer

&lt;400&gt; 11

cagcgttcca ctgacaccaa gacaatgg

28

20 &lt;210&gt; 12

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

25 &lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:Primer

&lt;400&gt; 12

30 aaggcgaaca ggtgggtgag gctaacc

27

&lt;210&gt; 13

&lt;211&gt; 20

&lt;212&gt; DNA

35 &lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:Primer

&lt;400&gt; 13

40 tggcgaaggc gaacaggtgg

20

&lt;210&gt; 14

45 &lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

50 &lt;223&gt; Description of Artificial Sequence:Primer

&lt;400&gt; 14

gcgaaggcga acaggtgggt gagg

24

55

SUBSTITUTE SHEET (RULE 26)



<210> 15  
<211> 24  
<212> DNA  
<213> Artificial Sequence

5

<220>  
<223> Description of Artificial Sequence:Primer

10

<400> 15  
ctagtgttgc agcgcaagcc gcag

24

<210> 16  
<211> 28  
<212> DNA  
<213> Artificial Sequence

15

<220>  
<223> Description of Artificial Sequence:Primer

20

<400> 16  
cacagaaagc ataaccagtg attgaacc

28

<210> 17  
<211> 27  
<212> DNA  
<213> Artificial Sequence

25

<220>  
<223> Description of Artificial Sequence:Primer

30

<400> 17  
gcttttaggtt cctggaatcc catttgg

27

<210> 18  
<211> 25  
<212> DNA  
<213> Artificial Sequence

40

<220>  
<223> Description of Artificial Sequence:Primer

45

<400> 18  
ttgtcaccag cataggcact gagtg

25